GGCATCTGCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGAGG $\tt CTCTGTTGAGAATC \textbf{ATG} \tt CTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTC$ CTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCC AGACTGCAGTAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGC CACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGT CATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGG GCAGCATGGCCCCAAAGGAGAGAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCAT TCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTT GAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGG TGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACC TTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGAT ACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGG CAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTG AAACTAAG**TAA**ATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGAT TTGTTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATT GGTTGCAATGTTGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAA GAATCAACCACAAAATAGTCTTCTCAGATGACCTTGACTAATATACTCAGCATCTTTATCAC TCTTTCCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTAT CACAGAAGTCATTTGCAAAGAATTTTGACTACTCTGCTTTTAATTTAATACCAGTTTTCAGG AACCCCTGAAGTTTTAAGTTCATTATTCTTTATAACATTTGAGAGAATCGGATGTAGTGATA TGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGCCCTCCG TGTTCAGCTTAGCCTTTGACCCTTTCCTTTTGATCCACAAAATACATTAAAACTCTGAATTC ACATACAATGCTATTTTAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGG TTGTAATTTTGTGTATGTTCCCCCACATCGCCCCCAACTTCGGATGTGGGGTCAGGAGGTTG AGGTTCACTATTAACAAATGTCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAA AGAGAAAGATTTTGACCTGGCTTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATAT ATGGAAATAAACACACCTTTGTTAAAGATAAAAAAAA

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><subunit 1 of 1, 246 aa, 1 stop

><MW: 26994, pI: 6.43, NX(S/T): 0

Important features of the protein:

Signal peptide:

amino acids 1-22

Motif name: Clq domain signature.

amino acids 137-167

Clq domain proteins.

amino acids 135-169, 202-221, 235-244, 57-91, 60-94, 54-88, 81-114, 78-111, 63-96, 51-84, 45-78, 48-81, 33-66, 66-99 and 42-75



GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTTGCAAGGCGACAGCTGTGCCAGCCGGG $\tt CTCTGGCAGGCTCCTGGCAGC \underline{ATG} GCAGTGAAGCTTGGGACCCTCCTGCTGGCCCTTGCCCT$ GGGCCTGCCCAGCCAGCCTCTGCCCGCAAGCTGCTGGTGTTTTCTGCTGGATGGTTTTC GCTCAGACTACATCAGTGATGAGGCGCTGGAGTCATTGCCTGGTTTCAAAGAGATTGTGAGC AGGGGAGTAAAAGTGGATTACTTGACTCCAGACTTCCCTAGTCTCTCGTATCCCAATTATTA TACCCTAATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACTACATGTGGGACC CCACCACCACCACGACTTTGACATTGGCGTCAACAAGACAGCCTAATGCCTCTCTGGTGG CTGGCCAGGCTGTGAGGTTGAGATTCTGGGTGTCAGACCCACCTACTGCCTAGAATATAAAA ATGTCCCAACGGATATCAATTTTGCCAATGCAGTCAGCGATGCTCTTGACTCCTTCAAGAGT GGCCGGGCCGACCTGGCAGCCATATACCATGAGCGCATTGACGTGGAAGGCCACCACTACGG GCCTGCATCTCCGCAGAGGAAAGATGCCCTCAAGGCTGTAGACACTGTCCTGAAGTACATGA CCAAGTGGATCCAGGAGCGGGCCTGCAGGACCGCCTGAACGTCATTATTTCTCGGATCAC GGAATGACCGACATTTTCTGGATGGACAAAGTGATTGAGCTGAATAAGTACATCAGCCTGAA ATCCCAAGCAGGTTCTATTACAAGAAAGGAAAGTTTGTCTCTCTTTGACTTTAGTGGCTGA TGAAGGCTGGTTCATAACTGAGAATCGAGAGATGCTTCCGTTTTGGATGAACAGCACCGGCA GGCGGGAAGGTTGGCAGCGTGGATGGCACGGCTACGACAACGAGCTCATGGACATGCGGGGC ATCTTCCTGGCCTTCGGACCTGATTTCAAATCCAACTTCAGAGCTGCTCCTATCAGGTCGGT GGACGTCTACAATGTCATGTGCAATGTGGTGGGCATCACCCCGCTGCCCAACAACGGATCCT GGTCCAGGGTGATGTGCATGCTGAAGGGCCGCCGCCGCACTGCCCCGCCTGTCTGGCCCAGC $\texttt{CACTGTGCCCTGGCACTGATTCTTCTCTTCTTGCTGCA} \underline{\textbf{TAA}} \texttt{CTGATCATATTGCTTGTCTC}$ AGAAAAAACACCATCAGCAAAGTGGGCCTCCAAAGCCAGATGATTTTCATTTTATGTGTGA ATAATAGCTTCATTAACACAATCAAGACCATGCACATTGTAAATACATTATTCTTGGATAAT

TCTATACATAAAAGTTCCTACTTGTTAAA

MAVKLGTLLLALALGLAQPASARRKLLVFLLDGFRSDYISDEALESLPGFKEIVSRGVKVDY
LTPDFPSLSYPNYYTLMTGRHCEVHQMIGNYMWDPTTNKSFDIGVNKDSLMPLWWNGSEPLW
VTLTKAKRKVYMYYWPGCEVEILGVRPTYCLEYKNVPTDINFANAVSDALDSFKSGRADLAA
IYHERIDVEGHHYGPASPQRKDALKAVDTVLKYMTKWIQERGLQDRLNVIIFSDHGMTDIFW
MDKVIELNKYISLNDLQQVKDRGPVVSLWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFYY
KKGKFVSPLTLVADEGWFITENREMLPFWMNSTGRREGWQRGWHGYDNELMDMRGIFLAFGP
DFKSNFRAAPIRSVDVYNVMCNVVGITPLPNNGSWSRVMCMLKGRAGTAPPVWPSHCALALI
LLFLLA

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 100-104, 118-122, 341-345, 404-408

N-myristoylation sites.

amino acids 148-154, 365-371

Amidation site.

amino acids 343-347

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCGCTGCCGCCACCATGACGCTCCTCC GGGCACCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCTCGGCCA GGCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGG TGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAG CTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGT GCCTGTGCAGAGGCTGTATCGATGCACGGACGGCCGCGAGACAGCTGCGCTCAACTCCGTG CGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCT CCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCT GCGTGCTGCCCCGTTCAGTG**TGA**CCGCCGAGGCCGTGGGGCCCCTAGACTGGACACGTGTGC ACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTCTCCTCATCTC CAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGCCCTTAAAGCTGCAGAA AAGGTGTCACACGGCTGCCTGTACCTTGGCTCCCTGTCCTGCTCCCGGCTTCCCTTACCCTA TCACTGGCCTCAGGCCCGCAGGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCT TAAACAATTATTTAAGTGTACGTGTATTATTAAACTGATGAACACATCCCCAAAA

MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQAL PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRYPQKL AFAECLCRGCIDARTGRETAALNSVRLLQSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVP VGCTCVLPRSV

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 112-121

N-myristoylation sites.

amino acids 32-38, 55-61, 133-139

Leucine zipper pattern.

amino acids 3-25

Homologous region to IL-17.

amino acids 99-195

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77623

><subunit 1 of 1, 97 aa, 1 stop

><MW: 10160, pI: 6.56, NX(S/T): 0

 ${\tt MQLGTGLLLAAVLSLQLAAAEAIWCHQCTGFGGCSHGSRCLRDSTHCVTTATRVLSNTEDLP} \\ {\tt LVTKMCHIGCPDIPSLGLGPYVSIACCQTSLCNHD}$

Important features of the protein:

Signal peptide:

amino acids 1-20

N-myristoylation sites.

amino acids 6-11 and 33-38

Prokaryotic membrane lipoprotein lipid attachment sites.

amino acids 24-34 and 78-88

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCAGAGGCCGGGGAAGAGAAAGCAAAG CGCAACGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCCT AACTTCAGTCCCCCAAACGCGCACCCTCGAAGTCTTGAACTCCAGCCCCGCACATCCACGCG CGGCACAGGCGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTCGGGCAG CTGGGCTCGGGCGGGAGTAGGGCCCGGCAGGGAGGCAGGGAGGCTGCATATTCAGAGTC GCGGGCTGCGCCCTGGGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCG CCGCG**ATG**AGCCGCGTGGTCTCGCTGCTGGGCGCCGCCGCTCTCTGCGGCCACGGAGCC TTCTGCCGCCGCGTGGTCAGCGGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTA CAAAATGGCCTACTTCCATGAACTGTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCTGGCTT GTGAGAGTGAGGGAGGGCTCCTCCTCAGCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAG AGCATGTTGCAAAACCTGACAAAACCCGGGACAGGGATTTCTGATGGTGATTTCTGGATAGG ATGGAAGCAATTCCCAGTACCGAAACTGGTACACAGATGAACCTTCCTGCGGAAGTGAAAAG TGTGTTGTGATGTATCACCAACCAACTGCCAATCCTGGCCTTGGGGGTCCCTACCTTTACCA GTGGAATGATGACAGGTGTAACATGAAGCACAATTATATTTGCAAGTATGAACCAGAGATTA ATCCAACAGCCCCTGTAGAAAAGCCTTATCTTACAAATCAACCAGGAGACACCCATCAGAAT GTGGTTGTTACTGAAGCAGGTATAATTCCCAATCTAATTTATGTTGTTATACCAACAATACC CCTGCTCTTACTGATACTGGTTGCTTTTGGAACCTGTTGTTTCCAGATGCTGCATAAAAGTA AAGGAAGAACAAAACTAGTCCAAACCAGTCTACACTGTGGATTTCAAAGAGTACCAGAAAA GAAAGTGGCATGGAAGTA<u>TAA</u>TAACTCATTGACTTGGTTCCAGAATTTTGTAATTCTGGATC TGTATAAGGAATGGCATCAGAACAATAGCTTGGAATGGCTTGAAATCACAAAGGATCTGCAA GATGAACTGTAAGCTCCCCCTTGAGGCAAATATTAAAGTAATTTTTATATGTCTATTATTTC ATTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCAC CCAAACTTCAAACTTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTC GGGAGTATGTGTTAGAAGCAATTCCTTTTATTTCTTTCACCTTTCATAAGTTGTTATCTA GTCAATGTAATGTATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAA TACCATAGAAAAAGTTTGTTTTCTCGAAATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCA ATGTCTAGGAAATCTCTTCAGAAATAAGAAGCTATTTCATTAAGTGTGATATAAACCTCCTC AAACATTTTACTTAGAGGCAAGGATTGTCTAATTTCAATTGTGCAAGACATGTGCCTTATAA TTATTTTTAGCTTAAAATTAAACAGATTTTGTAATAATGTAACTTTGTTAATAGGTGCATAA ACACTAATGCAGTCAATTTGAACAAAAGAAGTGACATACACAATATAAATCATATGTCTTCA CACGTTGCCTATATAATGAGAAGCAGCTCTCTGAGGGTTCTGAAATCAATGTGGTCCCTCTC TTGCCCACTAAACAAGATGGTTGTTCGGGGTTTGGGATTGACACTGGAGGCAGATAGTTGC AAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGCCTCTGACTATATTAGTATACAAAGAGG TCATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAGACAAGCACAGCACAGAC ATTTTAGGAAGGAAGGAACTACGAAATCGTGTGAAAATGGGTTGGAACCCATCAGTGATCG CATATTCATTGATGAGGGTTTGCTTGAGATAGAAAATGGTGGCTCCTTTCTGTCTTATCTCC TAGTTTCTTCAATGCTTACGCCTTGTTCTTCTCAAGAGAAAGTTGTAACTCTCTGGTCTTCA

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><subunit 1 of 1, 273 aa, 1 stop

><MW: 30431, pI: 6.79, NX(S/T): 3

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Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89 and 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145 and 212-217

CCACAGCCACTGGGCCCGAAGTTGCTCAGCCTGAAGTAGACACCACCTGGGTCGTGTGCGAGGCCGGCAGGTGG GCGTGAAGGGCACAGACCGCCTTGTGAATGTCTTTCTGGGCATTCCATTTGCCCAGCCGCCACTGGGCCCTGACC GGTTCTCAGCCCCACACCCAGCACAGCCCTGGGAGGGTGTGCGGGATGCCAGCACTGCGCCCCCAATGTGCCTAC AAGACGTGGAGAGCATGAACAGCAGATTTGTCCTCAACGGAAAACAGCAGATCTTCTCCGTTTCAGAGGACT GCCTGGTCCTCAACGTCTATAGCCCAGCTGAGGTCCCCGCAGGGTCCGGTAGGCCGGTCATGGTATGGGTCCATG GAGGCGCTCTGATAACTGGCGCTGCCACCTCCTACGATGGATCAGCTCTGGCTGCCTATGGGGATGTGGTCGTGG TTACAGTCCAGTACCGCCTTGGGGTCCTTGGCTTCTTCAGCACTGGAGATGAGCATGCACCTGGCAACCAGGGCT TCCTAGATGTGGTAGCTGCTTTGCGCTGGGTGCAAGAAAACATCGCCCCCTTCGGGGGTGACCTCAACTGTGTCA CTGTCTTTGGTGGATCTGCCGGTGGGAGCATCATCTCTGGCCTGGTCCTGTCCCCAGTGGCTGCAGGGCTGTTCC ACAGAGCCATCACACAGAGTGGGGTCATCACCACCCCAGGGATCATCGACTCTCACCCTTGGCCCCTAGCTCAGA GCCCCAAGGAACTCCTGAAGGAGAAGCCCTTCCACTCTGTGCCCTTCCTCATGGGTGTCAACAACCATGAGTTCA GCTGGCTCATCCCCAGGGGCTGGGGTCTCCTGGATACAATGGAGCAGATGAGCCGGGAGGACATGCTGGCCATCT CAACACCCGTCTTGACCAGTCTGGATGTGCCCCCTGAGATGATGCCCACCGTCATAGATGAATACCTAGGAAGCA ACTCGGACGCACAAGCCAAATGCCAGGCGTTCCAGGAATTCATGGGTGACGTATTCATCAATGTTCCCACCGTCA GTTTTTCAAGATACCTTCGAGATTCTGGAAGCCCTGTCTTTTTCTATGAGTTCCAGCATCGACCCAGTTCTTTTG CGAAGATCAAACCTGCCTGGGTGAAGGCTGATCATGGGGCCGAGGGTGCTTTTGTGTTCGGAGGTCCCTTCCTCA TGGACGAGAGCTCCCGCCTGGCCTTTCCAGAGGCCACAGAGGAGGAGAAGCAGCTAAGCCTCACCATGATGGCCC AGTGGACCCACTTTGCCCGGACAGGGGACCCCAATAGCAAGGCTCTGCCTCCTTGGCCCCAATTCAACCAGGCGG AACAATATCTGGAGATCAACCCAGTGCCACGGGCCGGACAGAAGTTCAGGGAGGCCTGGATGCAGTTCTGGTCAG AGACGCTCCCCAGCAAGATACAACAGTGGCACCAGAAGCAGAAGAACAGGAAGGCCCAGGAGGACCTC**TGA**GGCC CCCCTGCTGAGACTTTAATCTCCACCAGCCCTTAAAGTGTCGGCCGCTCTGTGACTGGAGTTATGCTCTTTTGAA ${\tt ATGTCACAAGGCCGCCTCCCACCTCTGGGGCATTGTACAAGTTCTTCCCTCTCCCTGAAGTGCCTTTCCTGCTTT}$ CCCCCTCAGAGGAGCTCTCTCAAAATGGGGATTAGCCTAACCCCACTCTGTCACCCACACCAGGATCGGGTGGGA CCTGGAGCTAGGGGGTGTTTGCTGAGTGAGTGAGTGAACACAGAATATGGGAATGGCAGCTGCTGAACTTGAAC ${\tt CCAGAGCCTTCAGGTGCCAAAGCCATACTCAGGCCCCCACCGACATTGTCCACCCTGGCCAGAAGGGTGCATGCC}$ AATGGCAGAGACCTGGGATGGGAGAAGTCCTGGGGCGCCAGGGGATCCAGCCTAGAGCAGACCTTAGCCCCTGAC ATCCATCAGGGCCATGAGTGTCACCCAGACCTGACCCTCACCAATTCCAGCCCCTGACCCTCAGGACGCTGGATG ${\tt CCAGCTCCCAGCCCCAGTGCCGGGTCCTCCCTTCCTTGGGGAGACCAGTTTCTGGGGAGCTTCCAAGCCCCCAGCCCCAGTGCCGGGGGGCCTTCCAAGCCCAGGCCCAGTTCCAAGCCCAGGCCCAGGTGCCGGGAGCTTCCAAGCCCCAGGCCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCCAGGCCAGGCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCAGGCCAGGCCAGGCCAGGCAGGCCAGGCAGGCCAGGCAGGCCAGGCCAGGCAGGCAGGCCAGGCCAGGCCAGGCAGGCAGGCCAGGCAG$ AGCACCCACCAAGACACAGCAGGACAGGCCAGGGGGAGGGCATCTGGACCAGGGCATCCGTCGGGCTATTGTCACA GAGAAAAGAAGAGACCCACCCACTCGGGCTGCAAAAGGTGAAAAGCACCAAGAGGTTTTCAGATGGAAGTGAGAG GTGACAGTGTGCTGGCAGCCCTCACAGCCCTCGCTTGCTCCCTGCCGCCTCTGCCTGGGCTCCCACTTTGGCA GCACTTGAGGAGCCCTTCAACCCGCCGCTGCACTGTAGGAGCCCCTTTCTGGGCTGGCCAAGGCCGGAGCCAGCT TAGCACCTGGGCCAGCAGCTGCTGTGCTCGATTTCTCGCTGGGCCTTAGCTGCCTCCCCGCGGGGCAGGGCTCGG GACCTGCAGCCCTCCATGCCTGACCCTCCCCCACCCCCGTGGGCTCCTGTGCGGCCGGAGCCTCCCCAAGGAG CGCCGCCCCTGCTCCACAGCGCCCAGTCCCATCGACCACCCAAGGGCTGAGGAGTGCGGGTGCACAGCGCGGGA GGACTTGGAGAACCTTTATGTCTAGCTAAGGGATTGTAAATACACCGATGGGCACTCTGTATCTAGCTCAAGGTT TGTAAACACCACCAATCAGCACCCTGTGTCTAGCTCAGTGTTTTGTGAATGCACCAATCCACACTCTGTATCTGGCT ACTCTGGTGGGGACTTGGAGAACCTTTGTGTCCACACTCTGTATCTAGCTAATCTAGTGGGGATGTGGAGAACCT TTGTGTCTAGCTCAGGGATCGTAAACGCACCAATCAGCACCCTGTCAAAACAGACCACTTGACTCTCTGTAAAAT GGACCAATCAGCAGGATGTGGGTGGGGCGAGACAAGAGAATAAAAGCAGGCTGCCTGAGCCAGCAGTGACAACCC CCCTCGGGTCCCCTCCCACGCCGTGGAAGCTTTGTTCTTTCGCTCTTTTGCAATAAATCTTGCTACTGCCCAAAA

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><subunit 1 of 1, 571 aa, 1 stop

><MW: 62282, pI: 5.56, NX(S/T): 1

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LVLNVYSPAEVPAGSGRPVMVWVHGGALITGAATSYDGSALAAYGDVVVVTVQYRLGVLGFF
STGDEHAPGNQGFLDVVAALRWVQENIAPFGGDLNCVTVFGGSAGGSIISGLVLSPVAAGLF
HRAITQSGVITTPGIIDSHPWPLAQKIANTLACSSSSPAEMVQCLQQKEGEELVLSKKLKNT
IYPLTVDGTVFPKSPKELLKEKPFHSVPFLMGVNNHEFSWLIPRGWGLLDTMEQMSREDMLA
ISTPVLTSLDVPPEMMPTVIDEYLGSNSDAQAKCQAFQEFMGDVFINVPTVSFSRYLRDSGS
PVFFYEFQHRPSSFAKIKPAWVKADHGAEGAFVFGGPFLMDESSRLAFPEATEEEKQLSLTM
MAQWTHFARTGDPNSKALPPWPQFNQAEQYLEINPVPRAGQKFREAWMQFWSETLPSKIQQW
HQKQKNRKAQEDL

Important features of the protein:

Signal peptide:

amino acids 1-27.

Transmembrane domain:

amino acids 226-245

N-glycosylation site.

amino acids 105-109

N-myristoylation sites.

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161, 162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363, 461-467

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 12-23

Carboxylesterases type-B serine active site.

amino acids 216-232

CATGGAGCCTCTTGCAGCTTACCCGCTAAAATGTTCCGGGCCCAGAGCAAAGGTATTTGCAG TTTTGCTGTCTATAGTTCTATGCACAGTAACGCTATTTCTTCTACAACTAAAATTCCTCAAA CCTAAAATCAACAGCTTTTATGCCTTTGAAGTGAAGGATGCAAAAGGAAGAACTGTTTCTCT GGAAAAGTATAAAGGCAAAGTTTCACTAGTTGTAAACGTGGCCAGTGACTGCCAACTCACAG ACAGAAATTACTTAGGGCTGAAGGAACTGCACAAAGAGTTTGGACCATCCCACTTCAGCGTG TTTTGCAAGAAAAACTACGGAGTAACTTTCCCCATCTTCCACAAGATTAAGATTCTAGGAT CTGAAGGAGAACCTGCATTTAGATTTCTTGTTGATTCTTCAAAGAAGGAACCAAGGTGGAAT TTTTGGAAGTATCTTGTCAACCCTGAGGGTCAAGTTGTGAAGTTCTGGAGGCCAGAGGAGCC AGGATCTA**TGA**GAATGCCATTGCGTTTCTAATAGAACAGAGAAATGTCTCCATGAGGGTTTG GTCTCATTTTAAACATTTTTTTTTTGGAGACAGTGTCTCACTCTGTCACCCAGGCTGGAGTG CAGTAGTGCGTTCTCAGCTCATTGCAACCTCTGCCTTTTTAAACATGCTATTAAATGTGGCA GATGTTACCCAAAGCAAAAATCAAGAGTAGCCAAAGAATCAACATGAAATATATTAACTACT TCCTCTGACCATACTAAAGAATTCAGAATACACAGTGACCAATGTGCCTCAATATCTTATTG TTCAACTTGACATTTTCTAGGACTGTACTTGATGAAAATGCCAACACACTAGACCACTCTTT GGATTCAAGAGCACTGTGTATGACTGAAATTTCTGGAATAACTGTAAATGGTTATGTTAATG GAATAAAACACAAATGTTGAAAAATGTAAAATATATATACATAGATTCAAATCCTTATATAT ACTATAACTGTCACTATGTATGTAACTGACATATATAAATAGTCATTTATAAATGACCGTAT

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><subunit 1 of 1, 209 aa, 1 stop

><MW: 23909, pI: 9.68, NX(S/T): 0

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Important features of the protein:

Signal peptide:

amino acids 1-31

Glutathione peroxidases signature 2.

amino acids 104-112

Glutathione peroxidases.

amino acids 57-82

CTGGGGGGCCCCACGGCCTCTTTCCTGAGGAGCCGCCGCCGCTTAGCGTGGCCCCCAGGGACTACCTGAACCAC TATCCCGTGTTTGTGGGCAGCGGGCCCGGACGCCTGACCCCCGCAGAAGGTGCTGACGACCTCAACATCCAGCGA GTCCTGCGGGTCAACAGGACGCTGTTCATTGGGGACAGGGACAACCTCTACCGCGTAGAGCTGGAGCCCCCCACG TCCACGGAGCTGCGGTACCAGAGGAAGCTGACCTGGAGATCTAACCCCAGCGACATAAACGTGTGTCGGATGAAG GGCAAACAGGAGGGCGAGTGTCGAAACTTCGTAAAGGTGCTGCTCCTTCGGGACGAGTCCACGCTCTTTGTGTGC GGTTCCAACGCCTTCAACCCGGTGTGCGCCAACTACAGCATAGACACCCTGCAGCCCGTCGGAGACAACATCAGC GGTATGCCCGCTGCCCGTACGACCCCAAGCACGCÇAATGTTGCCCTCTTCTCTGACGGGATGCTCTTCACAGCT ACTGTTACCGACTTCCTAGCCATTGATGCTGTCATCTACCGCAGCCTCGGGGACAGGCCCACCCTGCGCACCGTG TTCCGGGAGATTGCGATGGAGTTTAACTACCTGGAGAAGGTGGTGGTGTCCCGCGTGGCCCGAGTGTGCAAGAAC ${\tt GTCCTGGCCGTTTTTTCCACGCCCAGCAACAGCATCCCTGGCTCGGCTGTCTGCGCCTTTGACCTGACACAGGTG}$ GCAGCTGTGTTTGAAGGCCGCTTCCGAGAGCAGAAGTCCCCCGAGTCCATCTGGACGCCGGTGCCGGAGGATCAG GTGCCTCGACCCCGGCCCGGGTGCTGCGCAGCCCCCGGGATGCAGTACAATGCCTCCAGCGCCTTGCCGGATGAC ATCCTCAACTTTGTCAAGACCCACCCTCTGATGGACGAGGCGGTGCCCTCGCTGGGCCCATGCGCCCTGGATCCTG CGGACCCTGATGAGGCACCAGCTGACTCGAGTGGCTGTGGACGTGGGAGCCGGCCCCTGGGGCAACCAGACCGTT GTCTTCCTGGGTTCTGAGGCGGGGACGGTCCTCAAGTTCCTCGTCCGGCCCAATGCCAGCACCTCAGGGACGTCT GGGCAGCGGCTGCTGAGCTTGGACCTGGACGCAGCTTCGGGGGGCCTGCTGCCTTCCCCCGCTGCGTGGTC CGAGTGCCTGTGGCTGCCAGCAGTACTCGGGGTGTATGAAGAACTGTATCGGCAGTCAGGACCCCTACTGC GGGTGGCCCCCGACGCTCCTGCATCTTCCTCAGCCCGGGCACCAGAGCCGCCTTTGAGCAGGACGTGTCCGGG GCCAGCACCTCAGGCTTAGGGGACTGCACAGGACTCCTGCGGGCCCAGCCTCTCCGAGGACCGCGGGGGCTGGTG TGGTTCGTGGGCCTCCGTGAGCGGCGGGAGCTGGCCCGGCGCAAGGACAAGGACGCCATCCTGGCGCACGGGGCG GGCGAGGCGGTGCTGAGCGTCAGCCGCCTGGGCGAGCGCAGGGCGCAGGGTCCCGGGGGCCGGGCGGAGGCGGT GGCGGTGGCGCCGGGGTTCCCCCGGAGGCCCTGCTGGCGCCCCTGATGCAGAACGGCTGGGCCAAGGCCACGCTG CTGCAGGGCGGGCCCACGACCTGGACTCGGGGCTGCTGCCCACGCCCGAGCAGACGCCGCTGCCGCAGAAGCGC TCCGCTTCATCCTCCTCCTGCTGCTGCCCCCCGGGCCCCCGAGCAGCCCCCCGCGCCTGGGGAGCCGACC $\verb|CCCTGGAGCCCGCCCGACGGCAGCCTGAGGAGGCCACTGGGCCCCCACGCCCCTCCGGCCGCCACCCTGCGC| \\$ GACTTGGCCCACCTCCTCCCCTATGGGGGGGGGGGACAGGACTGCGCCCCCGTGCCCTAGGCCGGGGGCCCCCCG ATGCCTTGGCAGTGCCAGCCACGGGAACCAGGAGCGAGAGACGGTGCCAGAACGCCGGGGCCCGGGGCAACTCCG AGTGGGTGCTCAAGTCCCCCCGCGACCCACCCGCGGAGTGGGGGGCCCCCTCCGCCACAAGGAAGCACCAGCAG TGGGCGTTGGCTGAGCCGACGCTGGGGCTTCCAGAAGGCCCGGGGGTCTCCGAGGTGCCGGTTAGGAGTTTGAAC ATACGGCCCCAGGGTGGTGAGAGTCCCATGCCACCCGTCCCCTTGTGACCTCCCCCCTATGACCTCCAGCTGA ${\tt CCATGCATGCCACGTGGCTGGGTCCTCTGCCCTCTTTGGAGTTTGCCTCCCCAGCCCCCTCCCCATCAAT}$

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><subunit 1 of 1, 888 aa, 1 stop

><MW: 95285, pI: 8.89, NX(S/T): 8

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Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 318-339, 598-617

N-glycosylation sites.

amino acids 74-78, 155-159, 167-171, 291-295, 386-390, 441-445, 462-466

Glycosaminoglycan attachment sites.

amino acids 51-55, 573-577

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation sites.

amino acids 21-27, 50-56, 189-195, 333-339, 382-388, 448-454, 490-496, 491-497, 508-514, 509-515, 531-537, 558-564, 569-575, 574-580, 580-586, 610-616, 643-649, 663-669, 666-672, 667-673, 668-674, 669-675, 670-676, 868-874, 879-885

AGCAACTCAAGTTCATCATTGTCCTGAGAGAGAGGAGCAGCGCGGTTCTCGGCCGGGACAGC AGAACGCCAGGGGACCCTCACCTGGGCGCGCCGGGGCACGGGCTTTGATTGTCCTGGGGTCG CGGAGACCCGCGCGCCTGCCCTGCACGCCGGGCGGCAACCTTTGCAGTCGCGTTGGCTGCTG CGATCGGCCGGCGGTCCCTGCCGAAGGCTCGGCTGCTTCTGTCCACCTCTTACACTTCTTC ATTTATCGGTGGATCATTTCGAGAGTCCGTCTTGTAA**ATG**TTTTGGCACTTTGCTACTTTATT GCTTCTTTCTGGCGACAGTTCCAGCACTCGCCGAGACCGGCGGAGAAAGGCAGCTGAGCCCG CTATATTCAGGCAGTGGATACATCAGGGAATAAATTCACATCTTCTCCAGGCGAAAAGGTCT TCCAGGTGAAAGTCTCAGCACCAGAGGAGCAATTCACTAGAGTTGGAGTCCAGGTTTTAGAC CGAAAAGATGGGTCCTTCATAGTAAGATACAGAATGTATGCAAGCTACAAAAATCTGAAGGT GGAAATTAAATTCCAAGGGCAACATGTGGCCAAATCCCCATATATTTTAAAAGGGCCGGTTT ACCATGAGAACTGTGACTGTCCTCTGCAAGATAGTGCAGCCTGGCTACGGGAGATGAACTGC CCTGAAACCATTGCTCAGATTCAGAGAGATCTGGCACATTTCCCTGCTGTGGATCCAGAAAA GATTGCAGTAGAAATCCCAAAAAGATTTGGACAGAGGCAGAGCCTATGTCACTACACCTTAA AGGATAACAAGGTTTATATCAAGACTCATGGTGAACATGTAGGTTTTAGAATTTTCATGGAT GCCATACTACTTTCTTTGACTAGAAAGGTGAAGATGCCAGATGTGGAGCTCTTTGTTAATTT GAAACCATGGGCCGGGTAAGTCTGGATATGATGTCCGTGCAAGCTAACACGGGTCCTCCCTG GGAAAGCAAAAATTCCACTGCCGTCTGGAGAGGGCGAGACAGCCGCAAAGAGAGACTCGAGC TGGTTAAACTCAGTAGAAAACACCCAGAACTCATAGACGCTGCTTTCACCAACTTTTTCTTC TTTAAACACGATGAAAACCTGTATGGTCCCATTGTGAAACATATTTCATTTTTTGATTTCTT CAAGCATAAGTATCAAATAAATATCGATGGCACTGTAGCAGCTTATCGCCTGCCATATTTGC TAGTTGGTGACAGTGTTGTGCTGAAGCAGGATTCCATCTACTATGAACATTTTTACAATGAG CTGCAGCCCTGGAAACACTACATTCCAGTTAAGAGCAACCTGAGCGATCTGCTAGAAAAACT TAAATGGGCGAAAGATCACGATGAAGAGGCCAAAAAGATAGCAAAAGCAGGACAAGAATTTG CAAGAAATAATCTCATGGGCGATGACATATTCTGTTATTTCAAACTTTTCCAGGAATAT GCCAATTTACAAGTGAGTGAGCCCCAAATCCGAGAGGGCATGAAAAGGGTAGAACCACAGAC TGAGGACGACCTCTTCCCTTGTACTTGCCATAGGAAAAAGACCAAAGATGAACTC**TGA**TATG CAAAATAACTTCTATTAGAATAATGGTGCTCTGAAGACTCTTCTTAACTAAAAAGAAGAATT TTTTTAAGTATTAATTCCATGGACAATATAAAATCTGTGTGATTGTTTGCAGTATGAAGACA CATTTCTACTTATGCAGTATTCTCATGACTGTACTTTAAAGTACATTTTTAGAATTTTATAA TAAAACCACCTTTATTTTAAAGGAAAAAA

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><subunit 1 of 1, 502 aa, 1 stop

>< MW: 58043, pI: 7.94, NX(S/T): 2

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PYILKGPVYHENCDCPLQDSAAWLREMNCPETIAQIQRDLAHFPAVDPEKIAVEIPKRFGQR
QSLCHYTLKDNKVYIKTHGEHVGFRIFMDAILLSLTRKVKMPDVELFVNLGDWPLEKKKSNS
NIHPIFSWCGSTDSKDIVMPTYDLTDSVLETMGRVSLDMMSVQANTGPPWESKNSTAVWRGR
DSRKERLELVKLSRKHPELIDAAFTNFFFFKHDENLYGPIVKHISFFDFFKHKYQINIDGTV
AAYRLPYLLVGDSVVLKQDSIYYEHFYNELQPWKHYIPVKSNLSDLLEKLKWAKDHDEEAKK
IAKAGQEFARNNLMGDDIFCYYFKLFQEYANLQVSEPQIREGMKRVEPQTEDDLFPCTCHRK
KTKDEL

Important features of the protein:

Signal peptide:

amino acids 1-17

N-glycosylation sites.

amino acids 302-306, 414-418

cAMP- and cGMP-dependent protein kinase phosphorylation sites. amino acids 243-247, 495-499

Tyrosine kinase phosphorylation site.

amino acids 341-348

N-myristoylation sites.

amino acids 59-65, 118-124, 184-190, 258-264, 370-376, 439-445

Endoplasmic reticulum targeting sequence.

amino acids 499-504

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGCGAGGCTCCAGGTGGGGTCGGTTCCGCATCCA GCCTAGCGTGTCCACGATGCGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGATCG AGAGCGGAACACGGAGCGGAGCCCCAGCGCCCGAACCCTCGGCTGGAGCCAGTTCTAACTG GACCACGCTGCCACCACCTCTCTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAG ATGATTTTGTGTTTTGGGTCAAAGGGTGTGAAATTTATGCCCTACACAACTTACCTTGTGGAA AAAGGAGCATCTCACAGTTTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAAT CAAGGCATTGATGACGGGGAGCCTTCCTGGCTTTGTCGACGTCATCAGGAACCTCAATTCTC CTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAAGCAGCTGGAAAAAGAATAGTCTTT TATGGAGATGAAACCTGGGTTAAATTATTCCCAAAGCATTTTGTGGAATATGATGGAACAAC CTCATTTTTCGTGTCAGATTACACAGAGGTGGATAATAATGTCACGAGGCATTTGGATAAAG TATTAAAAAGAGGAGATTGGGACATATTAATCCTCCACTACCTGGGGCTGGACCACATTGGC CACATTTCAGGGCCCAACAGCCCCCTGATTGGGCAGAAGCTGAGCGAGATGGACAGCGTGCT TTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACGGGGCCTCCTCCACCGAGGAG GTGAATACACCTCTGATTTTAATCAGTTCTGCGTTTGAAAGGAAACCCGGTGATATCCGACA TCCAAAGCACGTCCAA**TAG**ACGGATGTGGCTGCGACACTGGCGATAGCACTTGGCTTACCGA CAGTTGAGATTTTTACATTTGAATACAGTGCAGCTTAGTAAACTGTTGCAAGAGAATGTGCC GTCATATGAAAAAGATCCTGGGTTTGAGCAGTTTAAAATGTCAGAAAGATTGCATGGGAACT GGATCAGACTGTACTTGGAGGAAAAGCATTCAGAAGTCCTATTCAACCTGGGCTCCAAGGTT CTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCCA GTTCTCACCCTGCTCCTGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGT CCCACTGTCATCTCCTGGGTTTTCTCTGCTCTTTTATTTGGTGATCCTGGTTCTTTCGGCCG TTCACGTCATTGTGTGCACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCCTCTCGTGGCTG GCGGCAGGCTGCCTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGCTGG CAGTGCCCTGGACAGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCCAGGCCTCTGGG TGTCCCGACACAGGTGTTCACATCTGTGCTGTCAGGTCAGATGCCTCAGTTCTTGGAAAGCT AGGTTCCTGCGACTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTCACAGAGGAACAAGCCC CCCAGCTGAGGGGGTGTGTGAATCGGACAGCCTCCCAGCAGAGGTGTGGGAGCTGCAGCTGA GGGAAGAAGAGACAATCGGCCTGGACACTCAGGAGGGTCAAAAGGAGACTTGGTCGCACCAC CGTTTTCTGTTGGAATTCTTAGTCCTTGGCCTCGGACACCTTCATTCGTTAGCTGGGGAGTG GTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCACACTCAGATCCACAGAGCCCAGGATCAAG GGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCCACCCCAACCCTGCACAGCCCTCATC CCCTCTTGGCTTGAGCCGTCAGAGGCCCTGTGCTGAGTGTCTGACCGAGACACTCACAGCTT TGTCATCAGGGCACAGGCTTCCTCGGAGCCAGGATGATCTGTGCCACGCTTGCACCTCGGGC CCATCTGGGCTCATGCTCTCTCTCTGCTATTGAATTAGTACCTAGCTGCACACAGTATGTA GTTACCAAAAGAATAAACGGCAATAATTGAGAAAAAAA

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><subunit 1 of 1, 310 aa, 1 stop

><MW: 33875, pI: 7.08, NX(S/T): 2

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Important features of the protein:

Signal peptide:

amino acids 1-34

Transmembrane domain:

amino acids 58-76

N-glycosylation sites.

amino acids 56-60, 194-198

N-myristoylation sites.

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276, 275-281, 278-284

Amidation site.

amino acids 154-158

Cell attachment sequence.

amino acids 205-208

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576

><subunit 1 of 1, 251 aa, 1 stop

><MW: 26935, pI: 7.42, NX(S/T): 2

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Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

CCCACGCGTCCGGGACAGATGAACTTAAAAGAGAAGCTTTAGCTGCCAAAGATTGGGAAAGG GAAAGGACAAAAAAGACCCCTGGGCTACACGGCGTAGGTGCAGGGTTTCCTACTGCTGTTCT TTTATGCTGGGAGCTGTGGCTGTAACCAACTAGGAAATAACGTATGCAGCAGCT<u>ATG</u>GCTGT CCTTGGCAGGTTCTGGGTTTGGACGTTATTCGGTGACTGAGGAAACAGAGAAAGGATCCTTT GGTGGTTTCCGATGATAACAAACAATACCTGCTCCTGGATTCACATACCGGGAATTTGCTCA CAAATGAGAAACTGGACCGAGAGAAGCTGTGTGGCCCTAAAGAGCCCTGTATGCTGTATTTC CAAATTTTAATGGATGATCCCTTTCAGATTTACCGGGCTGAGCTGAGAGTCAGGGATATAAA TGATCACGCGCCAGTATTTCAGGACAAAGAAACAGTCTTAAAAATATCAGAAAATACAGCTG AAGGGACAGCATTTAGACTAGAAAGAGCACAGGATCCAGATGGAGGACTTAACGGTATCCAA AACTACACGATCAGCCCCAACTCTTTTTTCCATATTAACATTAGTGGCGGTGATGAAGGCAT GATATATCCAGAGCTAGTGTTGGACAAAGCACTGGATCGGGAGGAGCAGGGAGAGCTCAGCT TAACCCTCACAGCGCTGGATGGTGGGTCTCCATCCAGGTCTGGGACCTCTACTGTACGCATC GTTGTCTTGGACGTCAATGACAATGCCCCACAGTTTGCCCAGGCTCTGTATGAGACCCAGGC TCCAGAAAACAGCCCCATTGGGTTCCTTATTGTTAAGGTATGGGCAGAAGATGTAGACTCTG GAGTCAACGCGGAAGTATCCTATTCATTTTTTGATGCCTCAGAAAATATTCGAACGACCTTT CAAATCAATCCTTTTTCTGGGGAAATCTTTCTCAGAGAATTGCTTGATTATGAGTTAGTAAA TTCTTACAAAATAAATATACAGGCAATGGACGGTGGAGGCCTTTCTGCAAGATGTAGGGTTT TAGTGGAAGTATTGGACACCAATGACAATCCCCCTGAACTGATCGTATCATCATTTTCCAAC TCTGTTGCTGAGAATTCTCCTGAGACGCCGCTGGCTGTTTTTAAGATTAATGACAGAGACTC TGGAGAAAATGGAAAGATGGTTTGCTACATTCAAGAGAATCTGCCATTCCTACTAAAACCTT CTGTGGAGAATTTTTACATCCTAATTACAGAAGGCGCGCTGGACAGAGAGATCAGAGCCGAG TACAACATCACTATCACCGTCACTGACTTGGGGACACCCAGGCTGAAAACCGAGCACAACAT AACGGTCTGGTCTCCGACGTCAATGACAACGCCCCGCCTTCACCCCAAACCTCCTACACCC GACTCGGGCACCAACGCCCAGGTCACCTACTCGCTGCCGCCCCCAAGACCCGCACCTGCC CCTCGCCTCCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTCGCCCTCAGGTCGCTGG ACTACGAGGCCTGCAGGCTTTCGAGTTCCGCGTGGGCGCCACAGACCGCGGCTCCCCCGCG CTGAGCAGAGAGGCGCTGGTGCCGGTGCTGGTGCTGGACGCCAACGACAACTCGCCCTTCGT GCTGTACCCGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCCGAGC CGGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACGCCGACTCGGGCCAGAACGCCTGGCTG TCGTACCAGCTGCTCAAGGCCACGGAGCCCGGGCTGTTCGGTGTGTGGGCGCACAATGGGGA GGTGCGCACCGCCAGGCTGCTGAGCGAGCGCGACGCCAAGCACAGGCTCGTGGTGCTTG TCAAGGACAATGGCGAGCCTCCTCGCTCGGCCACCGCCACGCTGCACTTGCTCCTGGTGGAC GGCTTCTCCCAGCCCTACCTGCCTCTCCCGGAGGCGCCCCGGCCCAGGCCCAGGCCGAGGC CGACTTGCTCACCGTCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCTCTCT CGGTGCTCCTGTTCGTGGCGGTGCGGCTGTGCAGGAGGAGCAGGCGGCCTCGGTGGGTCGC TGCTCGGTGCCCGAGGGTCCTTTTCCAGGGCATCTGGTGGACGTGAGGGGCGCTGAGACCCT GTCCCAGAGCTACCAGTATGAGGTGTCTGACGGGAGGCCCCGGGACCAGTGAGTTCAAGT TCTTGAAACCAGTTATTTCGGATATTCAGGCACAGGGCCCTGGGAGGAAGGGTGAAGAAAAT TCCACCTTCCGAAATAGCTTTGGATTTAATATTCAG**TAA**AGTCTGTTTTTAGTTTCATATAC TTTTGGTGTGTTACATAGCCATGTTTCTATTAGTTTACTTTTAAATCTCAAATTTAAGTTAT TATGCAACTTCAAGCATTATTTCAAGTAGTATACCCCTGTGGTTTTACAATGTTTCATCAT AAGGTTTTAATTCTTTCCAACTGCCCAAGGAATTAATTACTATTATATCTCATTACAGAAAT CTGAGGTTTTGATTCATTTCAGAGCTTGCATCTCATGATTCTAATCACTTCTGTCTATAGTG TACTTGCTCTATTTAAGAAGGCATATCTACATTTCCAAACTCATTCTAACATTCTATATATT CGTGTTTGAAAACCATGTCATTTATTTCTACATCATGTATTTAAAAAGAAATATTTCTCTAC TACTATGCTCATGACAAAATGAAACAAAGCATATTGTGAGCAATACTGAACATCAATAATAC CCTTAGTTTATATCTTATTTTTTTTTTATCTTTAAGCATGCTACTTTTACTTGGCCAATATTTT CTTATGTTAACTTTTGCTGATGTATAAAACAGACTATGCCTTATAATTGAAATAAAATTATA

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><subunit 1 of 1, 800 aa, 1 stop

><MW: 87621, pI: 4.77, NX(S/T): 7

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Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 687-711

N-glycosylation sites.

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

Glycosaminoglycan attachment site.

amino acids 28-32

Tyrosine kinase phosphorylation sites.

amino acids 394-402, 578-585

N-myristoylation sites.

amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190, 217-223, 324-330, 325-331, 471-477, 568-574, 759-765

Amidation site.

amino acids 781-785

Aminoacyl-transfer RNA synthetases class-II signature 1.

amino acids 117-138

Cadherins extracellular repeated domain signature.

amino acids 121-132, 230-241, 335-346, 439-450, 549-560



GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCCTC GTCTTCCTTCCGGGGGACAACGTGGGTCAGGGCACAGAGAGATATTTAATGTCACCCTCTTG GGGCTTTCATGGGACTCCCTCTGCCACATTTTTTGGAGGTTGGGAAAGTTGCTAGAGGCTTC CTGCTGCTGCTGGAGCGCGCATGTTCTCCTCACCCTCCCCGCCCCCGGCGCTGTTAGAGAA CCATCGAGAGCGACTCTGTCCAGCCTGTGCCTCGCTTCAGACAAGAGCTCTTCAGAATGATG GCCGTGGCTGCGGACACGCTGCAGCGCCTGGGGGCCCGTGTGGCCTCGGTGGACATGGGTCC TCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCGTCATCCTGGCCGAACTGGGGA GCGATCCCACGAAAGGCACCGTGTGCTTCTACGGCCACTTGGACGTGCAGCCTGCTGACCGG GGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGGTAGACGGGAAACTTTATGGACG AGGAGCGACCAACAAAGGCCCTGTCTTGGCTTGGATCAATGCTGTGAGCGCCTTCAGAG CCCTGGAGCAAGATCTTCCTGTGAATATCAAATTCATCATTGAGGGGATGGAAGAGGCTGGC TCTGTTGCCCTGGAGGAACTTGTGGAAAAAGAAAAGGACCGATTCTTCTCTGGTGTGGACTA CATTGTAATTTCAGATAACCTGTGGATCAGCCAAAGGAAGCCAGCAATCACTTATGGAACCC GGGGGAACAGCTACTTCATGGTGGAGGTGAAATGCAGAGACCAGGATTTTCACTCAGGAACC TTTGGTGGCATCCTTCATGAACCAATGGCTGATCTGGTTGCTCTTCTCGGTAGCCTGGTAGA CTCGTCTGGTCATATCCTGGTCCCTGGAATCTATGATGAAGTGGTTCCTCTTACAGAAGAGG AAATAAATACATACAAAGCCATCCATCTAGACCTAGAAGAATACCGGAATAGCAGCCGGGTT GAGAAATTTCTGTTCGATACTAAGGAGGAGATTCTAATGCACCTCTGGAGGTACCCATCTCT TTCTATTCATGGGATCGAGGGCGCGTTTGATGAGCCTGGAACTAAAACAGTCATACCTGGCC GAGTTATAGGAAAATTTTCAATCCGTCTAGTCCCTCACATGAATGTGTCTGCGGTGGAAAAA CAGGTGACACGACATCTTGAAGATGTGTTCTCCAAAAGAAATAGTTCCAACAAGATGGTTGT TTCCATGACTCTAGGACTACACCCGTGGATTGCAAATATTGATGACACCCCAGTATCTCGCAG ATTCCAATTGCCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTGCTAATTCCGCTGGG AGCTGTTGATGATGGAGAACATTCGCAGAATGAGAAAATCAACAGGTGGAACTACATAGAGG GAACCAAATTATTTGCTGCCTTTTTCTTAGAGATGGCCCAGCTCCAT**TAA**TCACAAGAACCT TCTAGTCTGATCCACTGACAGATTCACCTCCCCCACATCCCTAGACAGGGATGGAAT GTAAATATCCAGAGAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAAATGTCTTG GGATATCTGGATCAGTAATAAAATATTTCAAAGGCACAGATGTTGGAAATGGTTTAAGGTCC CCCACTGCACACCTTCCTCAAGTCATAGCTGCTTGCAGCAACTTGATTTCCCCAAGTCCTGT GCAATAGCCCCAGGATTGGATTCCTTCCAACCTTTTAGCATATCTCCAACCTTGCAATTTGA TTGGCATAATCACTCCGGTTTGCTTTCTAGGTCCTCAAGTGCTCGTGACACATAATCATTCC ATCCAATGATCGCCTTTGCTTTACCACTCTTTCCTTTTATCATTAATAAAAATGTTGGTC AAAAAAAA



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Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

273-292

N-glycosylation sites.

amino acids 322-326, 382-386, 402-406

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 400-404

N-myristoylation sites.

amino acids 89-95, 119-125, 162-168, 197-203, 242-248, 263-269, 351-357

Cell attachment sequence.

amino acids 140-143

ArgE / dapE / ACY1 / CPG:

amino acids 156-167

CTCGGCTGGATTTAAGGTTGCCGCTAGCCGCCTGGGAATTTAAGGGACCCACACTACCTTCC CGAAGTTGAAGGCAAGCGGTGATTGTTTGTAGACGGCGCTTTGTC**ATG**GGACCTGTGCGGTT GGGAATATTGCTTTTCCTTTTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGAAGGAGG AGGACGATGACACAGAACGCTTGCCCAGCAAATGCGAAGTGTGTAAGCTGCTGAGCACAGAG CTACAGGCGGAACTGAGTCGCACCGGTCGATCTCGAGAGGTGCTGGAGCTGGGGCAGGTGCT GGATACAGGCAAGAGGAGAGACACGTGCCTTACAGCGTTTCAGAGACAAGGCTGGAAGAGG CCTTAGAGAATTTATGTGAGCGGATCCTGGACTATAGTGTTCACGCTGAGCGCAAGGGCTCA CTGAGATATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCTAGTGCAGAAGGG GGTGAAGGTGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCCAGCGTGGAGGTCACAT ACCTCAAGAAGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATTGTGGGAGACTGGTAC TTCCACCATCAGGAGCAGCCCCTACAAAATTTTCTCTGTGAAGGTCATGTGCTCCCAGCTGC TGAAACTGCATGTCTACAGGAAACTTGGACTGGAAAGGAGATCACAGATGGGGAAGAGAAAA ATGACCAAGACAGGAAGCCACCCCAAACTTGACCGAGAAGATCTT**TGA**CCCTTGCCTTTGAG CCCCAGGAGGGGAAGGGATCATGGAGAGCCCTCTAAAGCCTGCACTCTCCCTGCTCCACAG CTTTCAGGGTGTGTTTATGAGTGACTCCACCCAAGCTTGTAGCTGTTCTCTCCCATCTAACC TCAGGCAAGATCCTGGTGAAACAGCATGACATGGCTTCTGGGGTGGAGGGTGGGGGTGGAGG TCCTGCTCCTAGAGATGAACTCTATCCAGCCCCTTAATTGGCAGGTGTATGTGCTGACAGTA CTGAAAGCTTTCCTCTTTAACTGATCCCACCCCACCCAAAAGTCAGCAGTGGCACTGGAGC TGTGGGCTTTGGGGAAGTCACTTAGCTCCTTAAGGTCTGTTTTTAGACCCTTCCAAGGAAGA GGCCAGAACGGACATTCTCTGCGATCTATATACATTGCCTGTATCCAGGAGGCTACACACCA GCAAACCGTGAAGGAGAATGGGACACTGGGTCATGGCCTGGAGTTGCTGATAATTTAGGTGG GATAGATACTTGGTCTACTTAAGCTCAATGTAACCCAGAGCCCACCATATAGTTTTATAGGT GCTCAACTTTCTATATCGCTATTAAACTTTTTTTCTTTTTTCTA

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><MW: 28310, pI: 4.63, NX(S/T): 0

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Important features of the protein:

Signal peptide:

amino acids 1-21

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 106-110

N-myristoylation site.

amino acids 115-121

Amidation site.

amino acids 70-74

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92274

><subunit 1 of 1, 223 aa, 1 stop

><MW: 25402, pI: 8.14, NX(S/T): 1

MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKVVP DCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKGADLK KGKIQGQELSAYQAPSPPAHSGFHRYQFFVYLQEGKVISLLPKENKTRGSWKMDRFLNRFHL GEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQR

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 169-173

Tyrosine kinase phosphorylation site.

amino acids 59-68

N-myristoylation sites.

amino acids 54-60, 83-89, 130-136

Phosphatidylethanolamine signature.

amino acids 113-157

GTCGACCCACGCGTCCGAAGCTGCTGGAGCCACGATTCAGTCCCCTGGACTGTAGATAAAGA CCCTTTCTTGCCAGGTGCTGAGACAACCACACT**ATG**AGAGGCACTCCAGGAGACGCTGATGG TGGAGGAAGGCCGTCTATCAATCAATCACTGTTGCTGTTATCACATGCAAGTATCCAGAGG CTCTTGAGCAAGGCAGAGGGGATCCCATTTATTTGGGAATCCAGAATCCAGAAATGTGTTTG TATTGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCT GTATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACCT CCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCATTGCCTCCCAAGAGAGACCAGCCC ATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGAATTAAATATAAATGA **CTGA**ACTCAGCCTAGAGGTGGCAGCTTGGTCTTTGTCTTAAAGTTTCTGGTTCCCAATGTGT TTTCGTCTACATTTTCTTAGTGTCATTTTCACGCTGGTGCTGAGACAGGAGCAAGGCTGCTG TTATCATCTCATTTTATAATGAAGAAGAAGCAATTACTTCATAGCAACTGAAGAACAGGATG TGGCCTCAGAAGCAGGAGAGCTGGGTGGTATAAGGCTGTCCTCTCAAGCTGGTGCTGTAG GCCACAAGGCATCTGCATGAGTGACTTTAAGACTCAAAGACCCAAACACTGAGCTTTCTTCTA GGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGCATGACTAGCACA GAGCTGATCTCTGTTTCTGTTTTGCTTTATTCCCTCTTGGGATGATATCATCCAGTCTTTAT ATGTTGCCAATATACCTCATTGTGTGTAATAGAACCTTCTTAGCATTAAGACCTTGTAAACA AAAATAATTCTTGGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGC ATGACTAGCACAGAGCTGATCTCTGTTTCTGTTTTGCTTTATTCCCTCTTGGGATGATATCA TCCAGTCTTTATATGTTGCCAATATACCTCATTGTGTGTAATAGAACCTTCTTAGCATTAAG ACCTTGTAAACAAAAATAATTCTTGTGTTAAGTTAAATCATTTTTGTCCTAATTGTAATGTG TAATCTTAAAGTTAAATAAACTTTGTGTATTTATATAATAATAAAGCTAAAACTGATATAAA ATAAAGAAAGAGTAAACTG



MRGTPGDADGGGRAVYQSITVAVITCKYPEALEQGRGDPIYLGIQNPEMCLYCEKVGEQPTL QLKEQKIMDLYGQPEPVKPFLFYRAKTGRTSTLESVAFPDWFIASSKRDQPIILTSELGKSY NTAFELNIND

Signal sequence:

amino acids 1-17

N-myristoylation site.

amino acids 10-16

Cell attachment sequence.

amino acids 36-39

 $\tt GCGAGGCTGCACCAGCGCCTGGCACC{\color{red} {\bf ATG}} AGGACGCCTGGGCCTCTGCCCGTGCTGCTG$ CTCCTGGCGGGAGCCCCGCCGCGCGCCCACTCCCCGACCTGCTACTCCCGCATGCGGGC CCTGAGCCAGGAGATCACCCGCGACTTCAACCTCCTGCAGGTCTCGGAGCCCTCGGAGCCAT GTGTGAGATACCTGCCCAGGCTGTACCTGGACATACACAATTACTGTGTGCTGGACAAGCTG CGGGACTTTGTGGCCTCGCCCCGTGTTGGAAAGTGGCCCAGGTAGATTCCTTGAAGGACAA AGCACGGAAGCTGTACACCATCATGAACTCGTTCTGCAGGAGAGATTTGGTATTCCTGTTGG ATGACTGCAATGCCTTGGAATACCCAATCCCAGTGACTACGGTCCTGCCAGATCGTCAGCGC TAAGGGAACTGAGACCAGAGAAGAACCCAAGAGAACTAAAGTTATGTCAGCTACCCAGACT TAATGGGCCAGAGCCATGACCTCACAGGTCTTGTGTTAGTTGTATCTGAAACTGTTATGTA TCTCTCTACCTTCTGGAAAACAGGGCTGGTATTCCTACCCAGGAACCTCCTTTGAGCATAGA GTTAGCAACCATGCTTCTCATTCCCTTGACTCATGTCTTGCCAGGATGGTTAGATACACAGC ATGTTGATTTGGTCACTAAAAAGAAGAAAAGGACTAACAAGCTTCACTTTTATGAACAACTA TTTTGAGAACATGCACAATAGTATGTTTTTATTACTGGTTTAATGGAGTAATGGTACTTTTA TTCTTTCTTGATAGAAACCTGCTTACATTTAACCAAGCTTCTATTATGCCTTTTTCTAACAC AGACTTTCTTCACTGTCTTTCATTTAAAAAGAAATTAATGCTCTTAAGATATATTTTTACG TAGTGCTGACAGGACCCACTCTTTCATTGAAAGGTGATGAAAATCAAATAAAGAATCTCTTC **ACATGGA**



></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA93011

><subunit 1 of 1, 136 aa, 1 stop

><MW: 15577, pI: 8.88, NX(S/T): 0

MRTPGPLPVLLLLLAGAPAARPTPPTCYSRMRALSQEITRDFNLLQVSEPSEPCVRYLPRLY LDIHNYCVLDKLRDFVASPPCWKVAQVDSLKDKARKLYTIMNSFCRRDLVFLLDDCNALEYP IPVTTVLPDRQR

Important features of the protein:

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site.

amino acids 60-69

N-myristoylation site.

amino acids 16-22



GTCTCCGCGTCACAGGAACTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGA CTTGACTCCCGCGCCCCCAACCCTGCTTATCCCTTGACCGTCGAGTGTCAGAGATCCTGCA GCCGCCCAGTCCCGGCCCTCTCCCGCCCCACACCCCTCCTGGCTCTTCCTGTTTTTAC TCCTCCTTTTCATTCATAACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCA AGCCGAGCGTGGAAGA**ATG**GGGTTCCTCGGGACCGGCACTTGGATTCTGGTGTTAGTGCTCC CGATTCAAGCTTTCCCCAAACCTGGAGGAAGCCAAGACAAATCTCTACATAATAGAGAATTA AGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAGAAGACAAGATTAAAAAAAC ATATCCTCCAGAAAACAAGCCAGGTCAGAGCAACTATTCTTTTGTTGATAACTTGAACCTGC CTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACTGATCGATGA TTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCATC AACTAGACGGGACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTAT GAAGAAATGACAGAGCCGTGTTTGACAAGATTGTTTCTAAACTACTTAATCTCGGCCTTAT CACAGAAAGCCAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCT CAAAGGAAGCCAACAATTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAG GCTGGAAAAATACCAGAGAAAGTGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGG AGAAAACGATGAAACAGTATCTAACACATTAACCTTGACAAATGGCTTGGAAAGGAGAACTA AAACCTACAGTGAAGACAACTTTGAGGAACTCCAATATTTCCCAAATTTCTATGCGCTACTG ACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCTCCAGAAGAAGGTGTTT GCTACTGACAATATAAGCAAGCTTTTCCCAGCACCATCAGAGAAGAGTCATGAAGAAACAGA CAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAA AAGATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTAT TTGGAAGCCATCAGAAAAAATATTGAATGGTTGAAGAAAACATGACAAAAAAGGGAAATAAAGA AGATTATGACCTTTCAAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTGGAGA AAGGCATCCTTGACAAGGAAGAAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTG**TAA**AAA TGGCAAAAGATCCAGGAGTCTTTCAACTGTTTCAGAAAACATAATATAGCTTAAAACACTTC TAATTCTGTGATTAAAATTTTTTGACCCAAGGGTTATTAGAAAGTGCTGAATTTACAGTAGT TAACCTTTTACAAGTGGTTAAAACATAGCTTTCTTCCCGTAAAAACTATCTGAAAGTAAAGT TGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAA

MGFLGTGTWILVLVLPIQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPEN
KPGQSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTK
SGLDHKFQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQA
HTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDET
VSNTLTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFV
KMMVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFPAPSEKSHEETDSTKEE
AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLS
KMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL

N-glycosylation sites:

amino acids 68-71, 346-349, 350-353

Casein kinase II phosphorylation site:

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-341, 369-372, 382-385, 386-389, 387-390

N-myristoylation sites:

amino acids 143-148, 239-244



GTTGCTCCGGCGGCGCTCGGGGAGGGAGCCAGCCTAGGGCCTAGGCCCGGGCCACC**ATG** GCGCTGCCTCCAGGCCCAGCCGCCCTCCGGCACACACTGCTGCTCCTGCCAGCCCTTCTGAG CTCAGGTTGGGGGGAGTTGGAGCCACAAATAGATGGTCAGACCTGGGCTGAGCGGGCACTTC GGGAGAATGAACGCCACGCCTTCACCTGCCGGGTGGCAGGGGGGCCTGGCACCCCCAGATTG GCCTGGTATCTGGATGGACAGCTGCAGGAGGCCAGCACCTCAAGACTGCTGAGCGTGGGAGG GGAGGCCTTCTCTGGAGGCACCAGCACCTTCACTGTCACTGCCCATCGGGCCCAGCATGAGC TCAACTGCTCTCTGCAGGACCCCAGAAGTGGCCGATCAGCCAACGCCTCTGTCATCCTTAAT GTGCAATTCAAGCCAGAGATTGCCCAAGTCGGCGCCAAGTACCAGGAAGCTCAGGGCCCAGG CCTCCTGGTTGTCCTGTTTGCCCTGGTGCGTGCCAACCCGCCGGCCAATGTCACCTGGATCG ACCAGGATGGCCAGTGACTGTCAACACCTCTGACTTCCTGGTGCTGGATGCGCAGAACTAC CCCTGGCTCACCAACCACGGTGCAGCTGCAGCTCCGCAGCCTGGCACACACCTCTCGGT GGTGGCCACCAATGACGTGGGTGTCACCAGTGCGTCGCTTCCAGCCCCAGGCCCCTCCCGGC ACCCATCTCTGATATCAAGTGACTCCAACAACCTAAAACTCAACAACGTGCGCCTGCCACGG GAGAACATGTCCCTCCCGTCCAACCTTCAGCTCAATGACCTCACTCCAGATTCCAGAGCAGT GAAACCAGCAGACCGGCAGATGGCTCAGAACAACAGCCGGCCAGAGCTTCTGGACCCGGAGC GTGTCCAGCGTGAGCAGTGATGAGATCTGGCTC<u>TGA</u>GCCGAGGGCGAGACAGGAGTATTCTC CACGTGATGCATTTCACTGGGCTGTAACCCGCAGGGCACAGGTATCTTTGGCAAGGCTACC AGTTGGACGTAAGCCCCTCATGCTGACTCAGGGTGGGCCCTGCATGTGATGACTGGGCCCTT CCAGAGGGAGCTCTTTGGCCAGGGGTGTTCAGATGTCATCCAGCATCCAAGTGTGGCATGGC CTGCTGTATACCCCACCCCAGTACTCCACAGCACCTTGTACAGTAGGCATGGGGGGCGTGCCT GTGTGGGGGACAGGGGCCCTGCATGGATTTTCCTCCTATGCTATGTAGCCTTGTT CCCTCAGGTAAAATTTAGGACCCTGCTAGCTGTGCAGAACCCAATTGCCCTTTGCACAGAAA CCAACCCTGACCCAGCGGTACCGGCCAAGCACAAACGTCCTTTTTGCTGCACACGTCTCTG CCCTTCACTTCTCTCTGTCCCCACCTCCTCTTGGGAATTCTAGGTTACACGTTGGACC TTCTCTACTACTTCACTGGGCACTAGACTTTTCTATTGGCCTGTGCCATCGCCCAGTATTAG CACAAGTTAGGGAGGAAGAGGCAGGCGATGAGTCTAGTAGCACCCAGGACGGCTTGTAGCTA GGGCCCAGAGCCCTCTTTGTGGCTTCCCCACGTTTGGCCTTCTGGGATTCACTGTGAGTGTC CTGAGCTCTCGGGGTTGATGGTTTTTCTCTCAGCATGTCTCCTCCACCACGGGACCCCAGCC CTGACCAACCCATGGTTGCCTCATCAGCAGGAAGGTGCCCTTCCTGGAGGATGGTCGCCACA CCCAAAGTGACCTAAGAACACTTTAAAAAGCAACATGTAAATGATTGGAAATTAATATAGTA CAGAATATTTTTCCCTTGTTGAGATCTTCTTTTGTAATGTTTTTCATGTTACTGCCTAGG AAAAAAAAAAAAAAAAA

MALPPGPAALRHTLLLLPALLSSGWGELEPQIDGQTWAERALRENERHAFTCRVAGGPGTPR LAWYLDGQLQEASTSRLLSVGGEAFSGGTSTFTVTAHRAQHELNCSLQDPRSGRSANASVIL NVQFKPEIAQVGAKYQEAQGPGLLVVLFALVRANPPANVTWIDQDGPVTVNTSDFLVLDAQN YPWLTNHTVQLQLRSLAHNLSVVATNDVGVTSASLPAPGPSRHPSLISSDSNNLKLNNVRLP RENMSLPSNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLLTSQGFIRLPVLGYIY RVSSVSSDEIWL

N-glycosylation sites:

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209, 251-255, 280-284

Glycosaminoglycan attachment site:

amino acids 23-27

Casein kinase II phosphorylation sites:

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

N-myristoylation sites:

amino acids 34-40, 89-95, 215-221, 292-298, 293-299





></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96857

><subunit 1 of 1, 221 aa, 1 stop

><MW: 23598, pI: 6.96, NX(S/T): 0

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Important features of the protein:

Signal peptide:

amino acids 1-28

Glycosaminoglycan attachment site.

amino acids 62-66

N-myristoylation sites.

amino acids 16-22, 25-31, 27-33, 61-67, 71-77, 86-92, 87-93, 91-97, 190-196

Endoplasmic reticulum targeting sequence.

amino acids 218-223



GTTGCTATGTTGCCCAGGCTGGTCTTGAAGTGCCTTGACCTCCTAAAGTGTTGGAACCACAG ACGTGAGCCACTCCACCCAGCCTAAAACTTCATCTTCTTTGGATGAGATGAACACTTTTAAC AAGAGAACAGGACTCTATATAAATCGCTGTGGGCTCACCACCTCTAAGGAGGAGCACTGACT GAAGACAGAAAAATTGATGAACTGAAGAAGACATGGTCCATTATGCCTTACAAACTTACACA GTGCTTTGGGAATTCCAAAGTACTCAGTGGAGAGAGGTGTTTCAGGAGCCGTAGAGCCAGAT CGTCATC**ATG**TCTGCATTGTGGCTGCTGGGCCTCCTTGCCCTGATGGACTTGTCTGAAA GCAGCAACTGGGGATGCTATGGAAACATCCAAAGCCTGGACACCCCTGGAGCATCTTGTGGG AGACATGCCATACCTCCTGAAATATCAACCCATGATGCAAACCATTGGCCAAAAGTACTGCA TGGATCCTGCCGTGATCGCTGGTGTCTTGTCCAGGAAGTCTCCCGGTGACAAAATTCTGGTC AACATGGGCGATAGGACTAGCATGGTGCAGGACCCTGGCTCTCAAGCTCCCACATCCTGGAT TAGTGAGTCTCAGGTTTCCCAGACAACTGAAGTTCTGACTACTAGAATCAAAGAATCCAGA GGAGGTTTCCAACCTGGACCCTGACCAGTACCTGAGAGGTGGACTCTGTGCCTACAGTGGG GGTGCTGGCTATGTCCGAAGCAGCCAGGACCTGAGCTGTGACTTCTGCAATGATGTCCTTGC ACGAGCCAAGTACCTCAAGAGACATGGCTTC**TAA**CATCTCAGATGAAACCCAAGACCATGAT CACATATGCAGCCTCAAATGTTACACAGATAAAACTAGCCAAGGGCACCTGTAACTGGGAAT



></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96867

.><subunit 1 of 1, 194 aa, 1 stop

><MW: 21431, pI: 8.57, NX(S/T): 0

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Important features of the protein:

Signal peptide:

amino acids 1-19

N-myristoylation sites.

amino acids 23-29, 26-32, 35-41, 45-51, 50-56, 76-82, 156-162

Amidation site.

amino acids 40-44





></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96878

><subunit 1 of 1, 125 aa, 1 stop

><MW: 13821, pI: 8.60, NX(S/T): 2

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Important features of the protein:

Signal peptide:

amino acids 1-18

N-glycosylation sites.

amino acids 77-81, 88-92

N-myristoylation site.

amino acids 84-90

Ly-6 / u-PAR domain protein signature.

amino acids 85-98

ACCGCACCCAGGTTCGGCCGTAGGCGTCTGGCAGCCCGGCGCCATCTTCATCGAGCGCCAT TGCTGACCGCGGGCCCTGCCCTGGGCTGGAACGACCCTGACAGAATGTTGCTGCGGGATGTA AAAGCTCTTACCCTCCACTATGACCGCTATACCACCTCCCGCAGGCTGGATCCCATCCCACA GTTGAAATGTGTTGGAGGCACAGCTGGTTGTGATTCTTATACCCCAAAAGTCATACAGTGTC AGAACAAAGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCA TACAAATTTGGAAAAACTGTGGTGAGCTGTGAAGGCTATGAGTCCTCTGAAGACCAGTATGT ACTAAGAGGTTCTTGTGGCTTGGAGTATAATTTAGATTATACAGAACTTGGCCTGCAGAAAC TGAAGGAGTCTGGAAAGCAGCACGGCTTTGCCTCTTTCTCTGATTATTATTATAAGTGGTCC TCGGCGGATTCCTGTAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGGATCGCCTT TGTAGTCTATAAGCTGTTCCTGAGTGACGGGCAGTATTCTCCTCCACCGTACTCTGAGTATC CTCCATTTTCCCACCGTTACCAGAGATTCACCAACTCAGCAGGACCTCCTCCCCCAGGCTTT AAGTCTGAGTTCACAGGACCACAGAATACTGGCCATGGTGCAACTTCTGGTTTTTGGCAGTGC TTTTACAGGACAACAAGGATATGAAAATTCAGGACCAGGGTTCTGGACAGGCTTGGGAACTG GTGGAATACTAGGATATTTGTTTGGCAGCAATAGAGCGGCAACACCCTTCTCAGACTCGTGG TACTACCCGTCCTATCCTCCTACCCTGGCACGTGGAATAGGGCTTACTCACCCCTTCA TGGAGGCTCGGGCAGCTATTCGGTATGTTCAAACTCAGACACGAAAACCAGAACTGCATCAG GATATGGTGGTACCAGGAGACGA**TAA**AGTAGAAAGTTGGAGTCAAACACTGGATGCAGAAAT TTTGGATTTTTCATCACTTTCTCTTTAGAAAAAAGTACTACCTGTTAACAATTGGGAAAAG GGGATATTCAAAAGTTCTGTGGTGTTATGTCCAGTGTAGCTTTTTGTATTCTATTATTTGAG GCTAAAAGTTGATGTGACAAAATACTTATGTGTTGTATGTCAGTGTAACATGCAGATGTA TATTGCAGTTTTTGAAAGTGATCATTACTGTGGAATGCTAAAAATACATTAATTTCTAAAAC CTGTGATGCCCTAAGAAGCATTAAGAATGAAGGTGTTGTACTAATAGAAACTAAGTACAGAA AATTTCAGTTTTAGGTGGTTGTAGCTGATGAGTTATTACCTCATAGAGACTATAATATTCTA TTTGGTATTATTATTTGATGTTTGCTGTTCTTCAAACATTTAAATCAAGCTTTGGACTAA TTATGCTAATTTGTGAGTTCTGATCACTTTTGAGCTCTGAAGCTTTGAATCATTCAGTGGTG GAGATGGCCTTCTGGTAACTGAATATTACCTTCTGTAGGAAAAGGTGGAAAATAAGCATCTA TCATAAGAGGTAAAGGTCAAATTTTTCAACAAAAGTCTTTTAATAACAAAAGCATGCAGTTC TCTGTGAAATCTCAAATATTGTTGTAATAGTCTGTTTCAATCTTAAAAAGAATCA

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889

><subunit 1 of 1, 339 aa, 1 stop

><MW: 36975, pI: 7.85, NX(S/T): 1

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Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 171-190

N-glycosylation site.

amino acids 172-176

Glycosaminoglycan attachment sites.

amino acids 244-248, 259-263, 331-335

Tyrosine kinase phosphorylation site.

amino acids 98-106

N-myristoylation sites.

amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272, 270-276, 278-284, 312-318